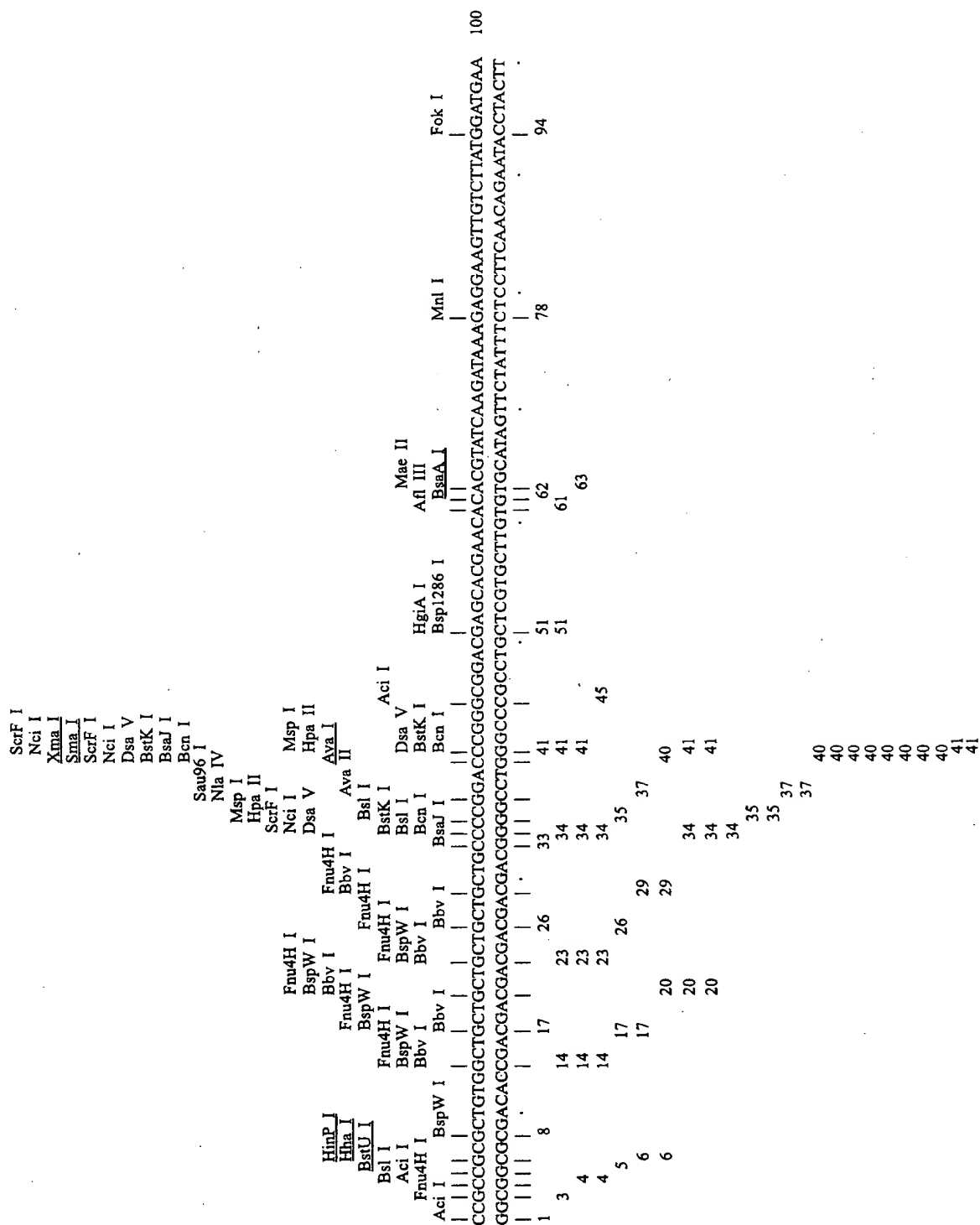


Fig. 19 A



Sau96 I
 Hae III
 Sau96 I
 Nla IV
 EcoO109 I
 Bsp1286 I
 Bsp120 I
 Ban II
 Apa I
 Rsa I
 Csp6 I
 Sca I
 Nla III
 108
 108
 108
 108
 108
 108
 108
 109
 109
 139
 140
 140
 192
 200
 207
 231
 250
 252
 255
 256
 269
 293
 315
 316
 316
 346
 349
 349
 349
 349
 350
 350
 358
 359
 359
 375
 393
 396
 400

Fig. 19 C

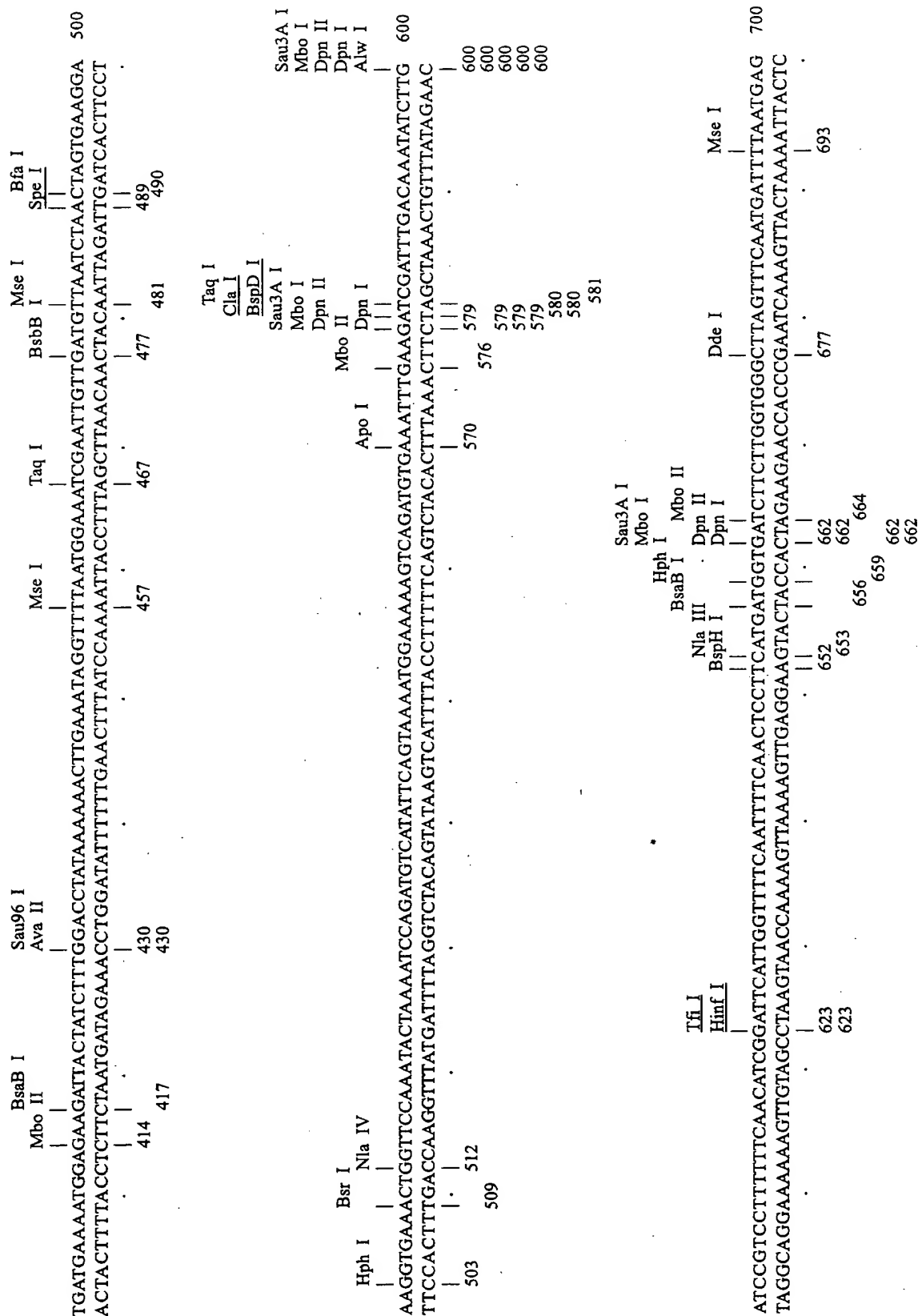


Fig. 19 D

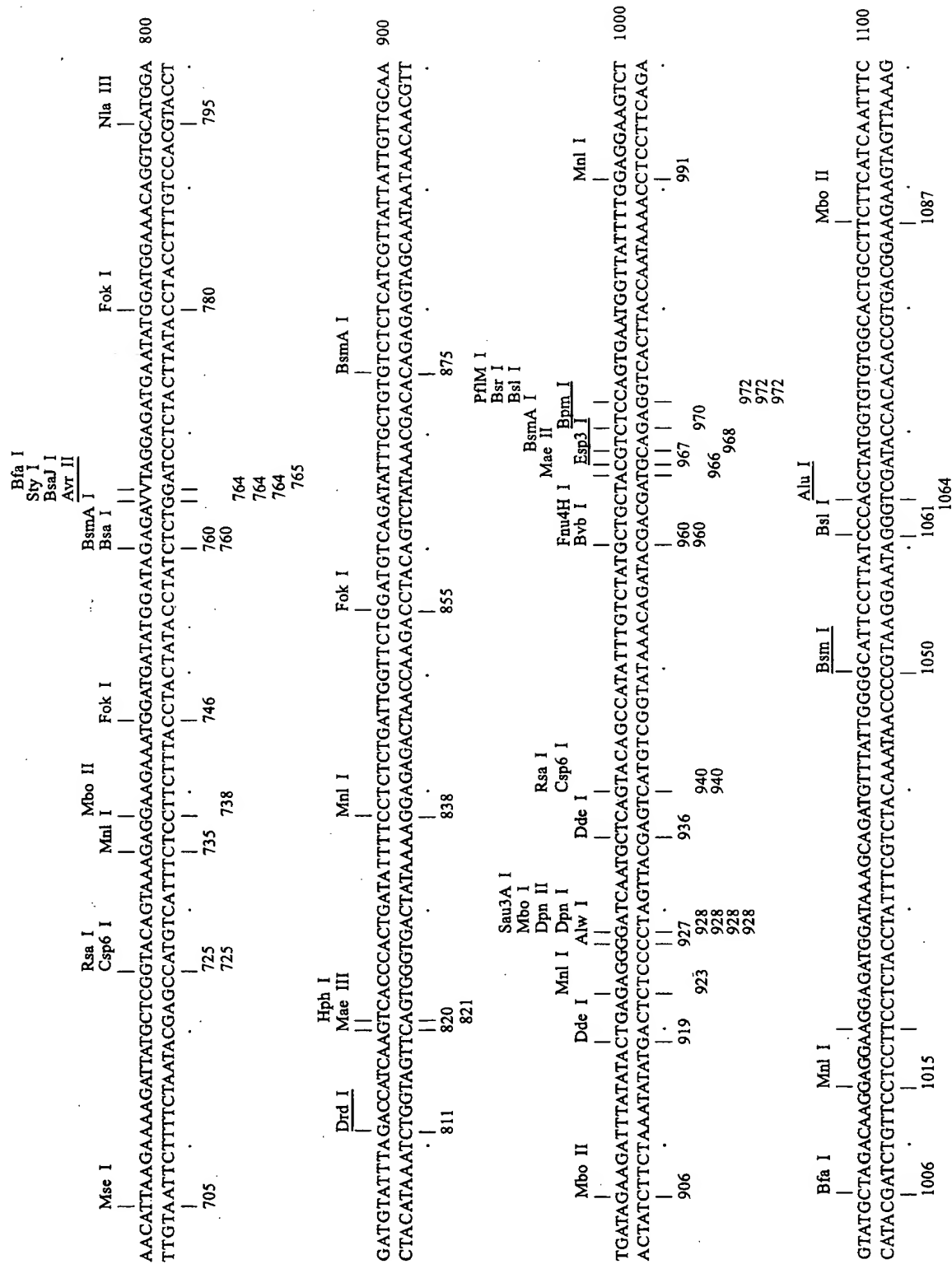


Fig. 19 E

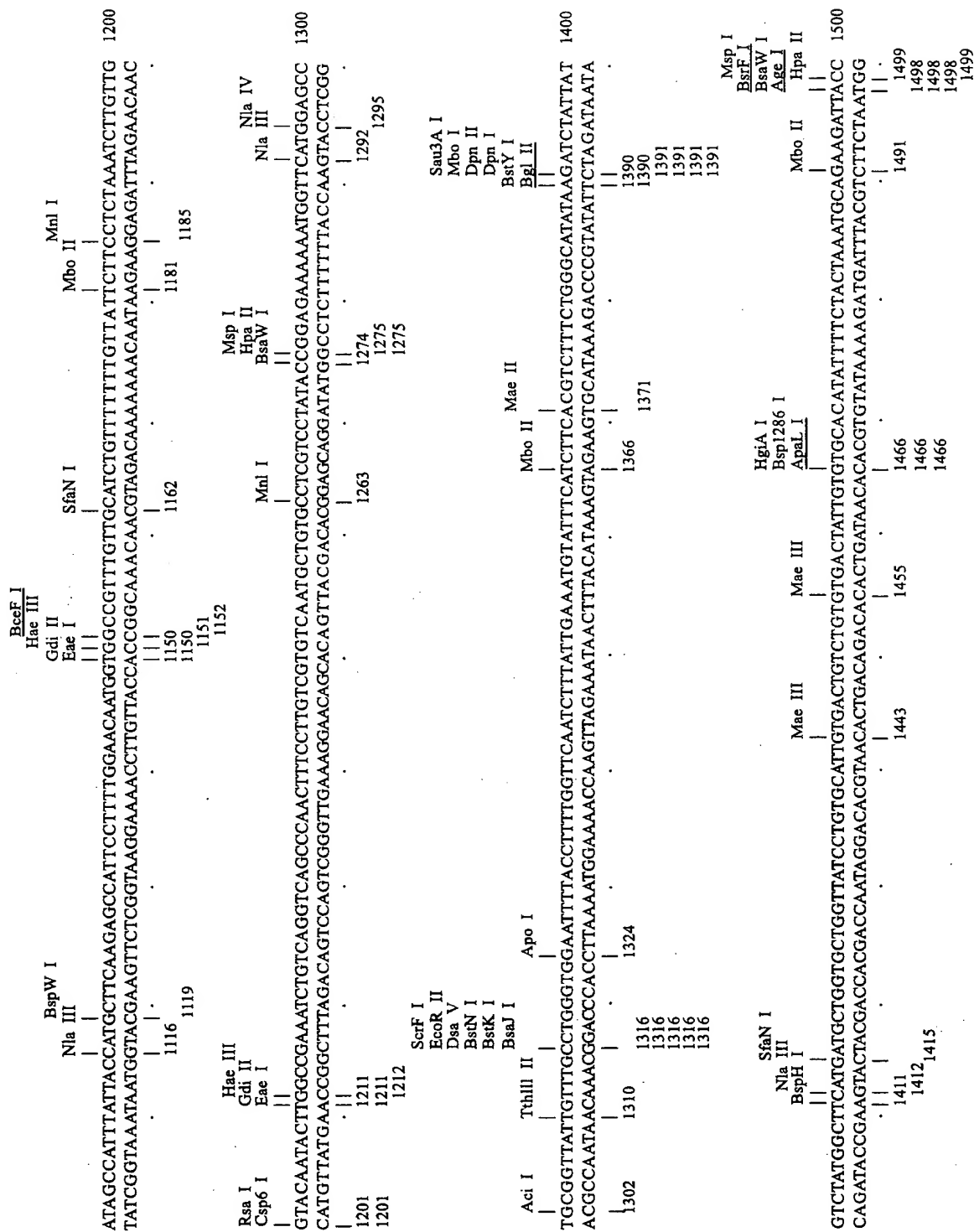


Fig. 19 F

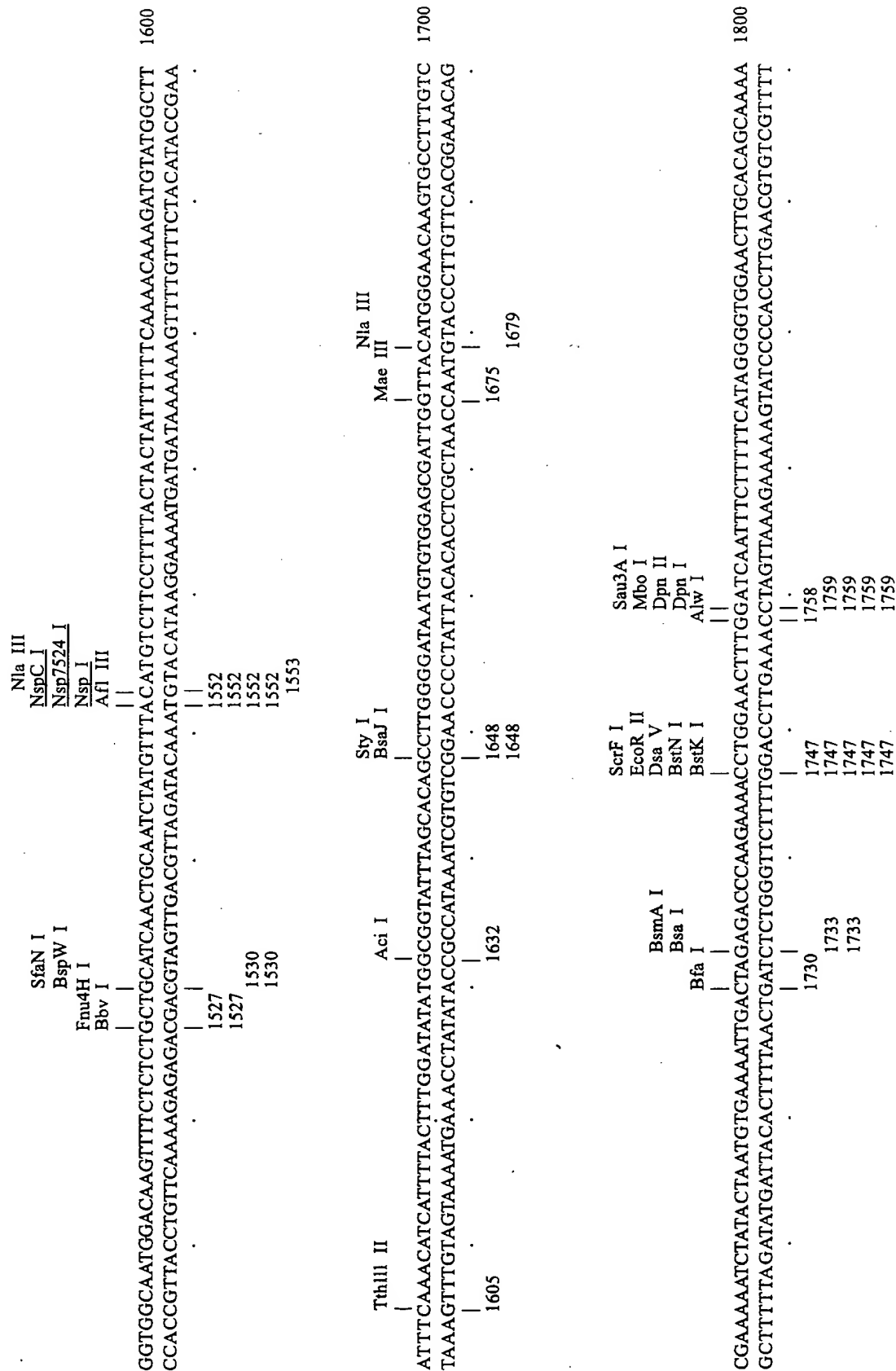


Fig. 22 A

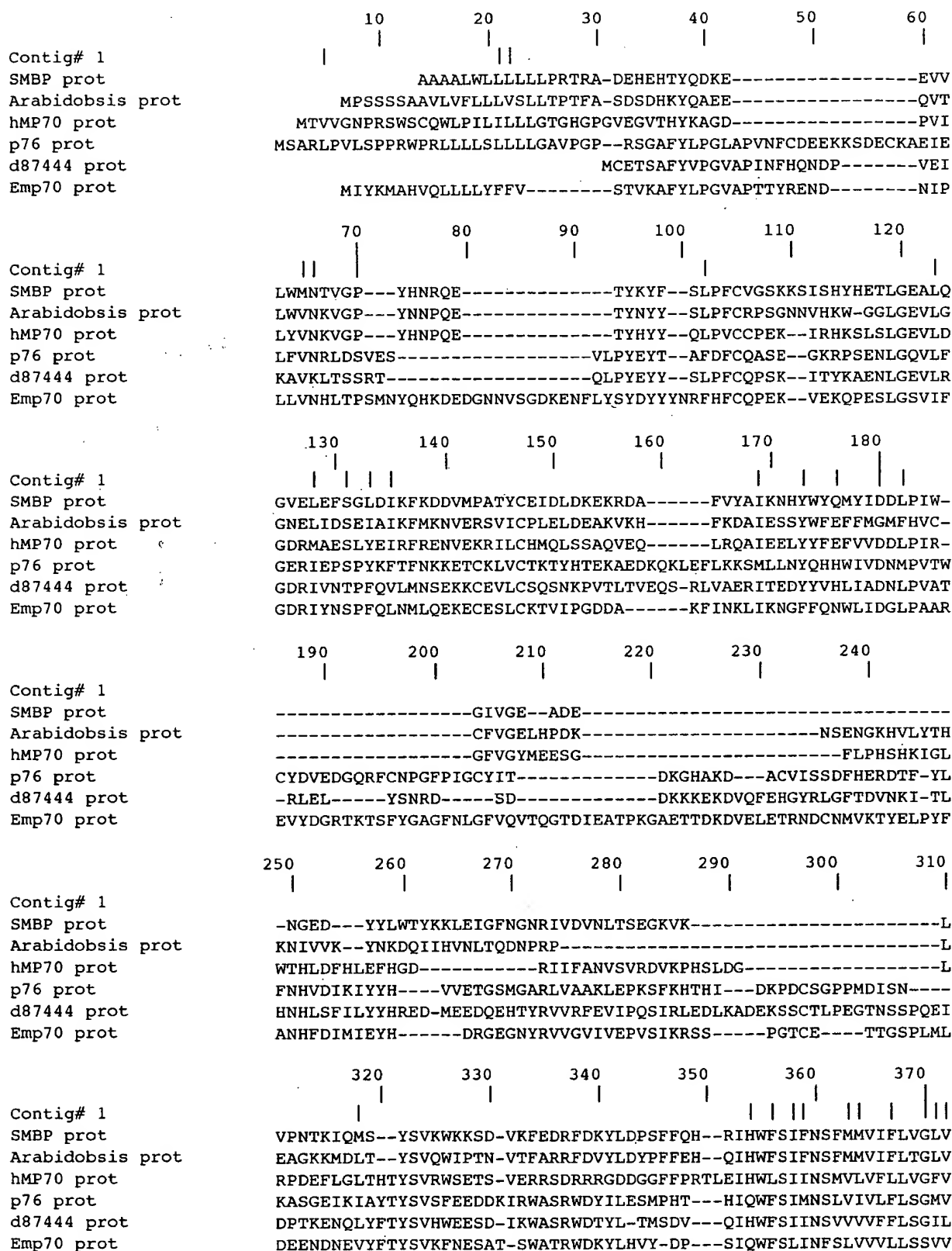


Fig. 22 B

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                                380      390      400      410      420      430
                                ||      |      |      |      |      |
Contig# 1                      ||      |      |      |      |      |
SMBP prot                     SMILMRTLRLKDYARTSKEEE-MDD-MDRDLGD-EGWKQVHGDVFRPSSHPLIFSSSLIGSGC
Arabidopsis prot              SMILMRTLRLNDYAKYAREDDDLLES-LERDVSE-ESGWKLVLHGDVFRPASSVLVLSAVVGTGA
hMP70 prot                    AVILMRVLRNLDLARYNLDEETTSAGSGDDDFDQGDNGWKIIHTDVFRFPPIYRGLLCAVLGSGA
p76 prot                      AMIMLRTLHLKDIARYNQ-----MDSTED-AQEEFGWKLVLHGDIFRPPRKGMLLSVFLGSGT
d87444 prot                   SMIIIRTLRKDIARYNKK-----LNDIED-TMEESGWKLVLHGDVFRPPQYOLMLSSLLGSGI
Emp70 prot                    IHSLLRALKDSDFARYNE-----LNLDDD-FQEDSGWKLNLHGDVFRSPSQSLTSLVVGSGV

```

440
450
460
470
480
490

Contig# 1
 SMBP prot QIFAVSLIVIIIVAMIEDLYTER-GSMLSTAIFVYAATSPVNGYFGGSLYARQGRRWIKQMF
 Arabidopsis prot QLALLVLLVILMAIVGTLYVGR-GAIVTTFIVCYALTSEFVSGYVSGGMYSRSGGKHWIKCMV
 hMP70 prot QFLALGTGIIVMALLGMFNVHRHGAINSAAILLYALTCCISGYVSSHFYRQIGGERWVWNII
 p76 prot QILIMTFVTLFFACLGFLSPANRGALMTCVVVLVWLLGTTPAGYVAAARFYKSFSGGEKWKTNVL
 d87444 prot QLFECMLIVIFVAMLGMLSPSSRGALMTTACFLFMFGVFGGFSAGRLYRTLKGHRWKKGA
 Emp70 prot QLFELMTCSIFFAALGFLSPSSRGSLATVMFILIYALFGFVGYSYTSMGIYKFFNPGPYWKANLI

500 510 520 530 540 550

Contig# 1
SMBP prot IGAFLIPAMVCGTAFFINFIAYYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLSG
Arabidopsis prot LTASLFPFLCFGIGFLLNTIAIFYGSLAAIPFGTMVVVFVIWGFISFPLALLGTVVGRNWSG
hMP70 prot: LTTSLSFVSPFFLTWSVVNSVHWANGSTQALPATTILLLLTVWLLVGFPPLTVIGGIFGKNNS
p76 prqt LTSFLCPGIVFADFFIMNLLIWGESSAAIPFGTLVAILALWFCISVPLTFIGAYGFKK-N
d87444 prot CTATLYPGVVFICFVNLNCFIWGKSSGAVPFPMTVALLCMWFCISLPLVYLGYYGFRRK-Q
Emp70 prot LTPLLVPGAILLIILNFFLMFVHSSGVIPASTLFFMVFLWFLFSIPSSFAGSLIARKRCH

560 570 580 590 600 610 620

Contig# 1
SMBP prot QPNFPCRVAVPRPIPEKKWFMEPAVIVCLGGILPFGSIFIEMYFIFTSEFWAYKIYYVYGFM
Arabidopsis prot APNNPCRVKTI PRPIPEKKWYLTSPVSLMGGLLPFGSIFIEMYFVFTSEFWNYKVYYVYGFM
hMP70 prot PFDAPCRTKNIAREINPQPWYKSTDIHMTVGGFLPFSAISVELYYIFATVWGREQYTYLGIL
p76 prot AIEHPVTRTNQIPRQIPEQSFYTKPLPGIIMGGILPFGCIFIQLEFFILNSIWSHQMYMFGFL
d87444 prot PYDNPVRTNQIPRQIPEQSWYMRNFVGIIMAGILPFGAMFIELEFFISAIWENQFYFLFGFL
Emp70 prot WDEHPTKTNQIARQIPFPWYLTIPATLIAGIFPFGSIAVELYFIYTSLWFNKIFYMFGFL

```

                                     630       640       650       660       670       680
Contig# 1      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
SMBP prot      MLVLVILCIVTVCVTIVCTYFLLNAEDYRWQWTSFLSAAST-AIYVVMYSFYIYFFKTKMYG
Arabidopsis prot LLVFVILVIVTVCVTIVGTYFLLNAENYHWQWTSFFSAAST-AVYVYLYSIYIYVVKTKMSG
hMP70 prot      FFVFAILLSVGASISIALTYFQLSGEDYRWWRWSVLSVGST-GLFIFLYSVFYIYARRSNMSG
p76 prot        FLVFIIILVTCSEATILLCYFHLCAEDYHWQWRSLTSGFT-AVYFLIYAVHYFFSKLQITG
d87444 prot     FLVFIIILVVSQSISIVMVYFQLCAEDYRWWRNFWLVSFSGGS-APYVLVYAIIFYFVNKLDIVE
Emp74 prot      FFSFLLLTLTSSLVTLITYLTHSLCLLENWKWOWRGFIIGGAGCALYVFIHSLF--TKFKLGG

```

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                                690      700      710      720
                                |        |        |        |
Contig# 1                      |        |        ||       |||      |
SMBP prot                      |        |        ||       |||      |
Arabidopsis prot              FFQTSFYFGYTMFMFCLGLGILCGAVGYLGSNLFVRRRIYRNIKCD
hMP70 prot                    AVQTFVEFFGYSLLTGYVFFLMLGTISFFSSLKFIRIYIVNLKMD
p76 prot                      TASTILYFGYTMIMVLIFLFTGTIGTIGFFACFWFVKTIYSVVKVD
d87444 prot                   FIPSLLYFGYGTALMVLFSWLLTGTIGTIGFYAAYMFVRKIYAAVKID
Emp70 prot                    FTTIVLVYVGYSVVISLLCCLVTGSIGFISSMLFVRKIYSSIKVD

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Fig. 23 A

Hydropathy index (Kyte-Doolittle, 1982)

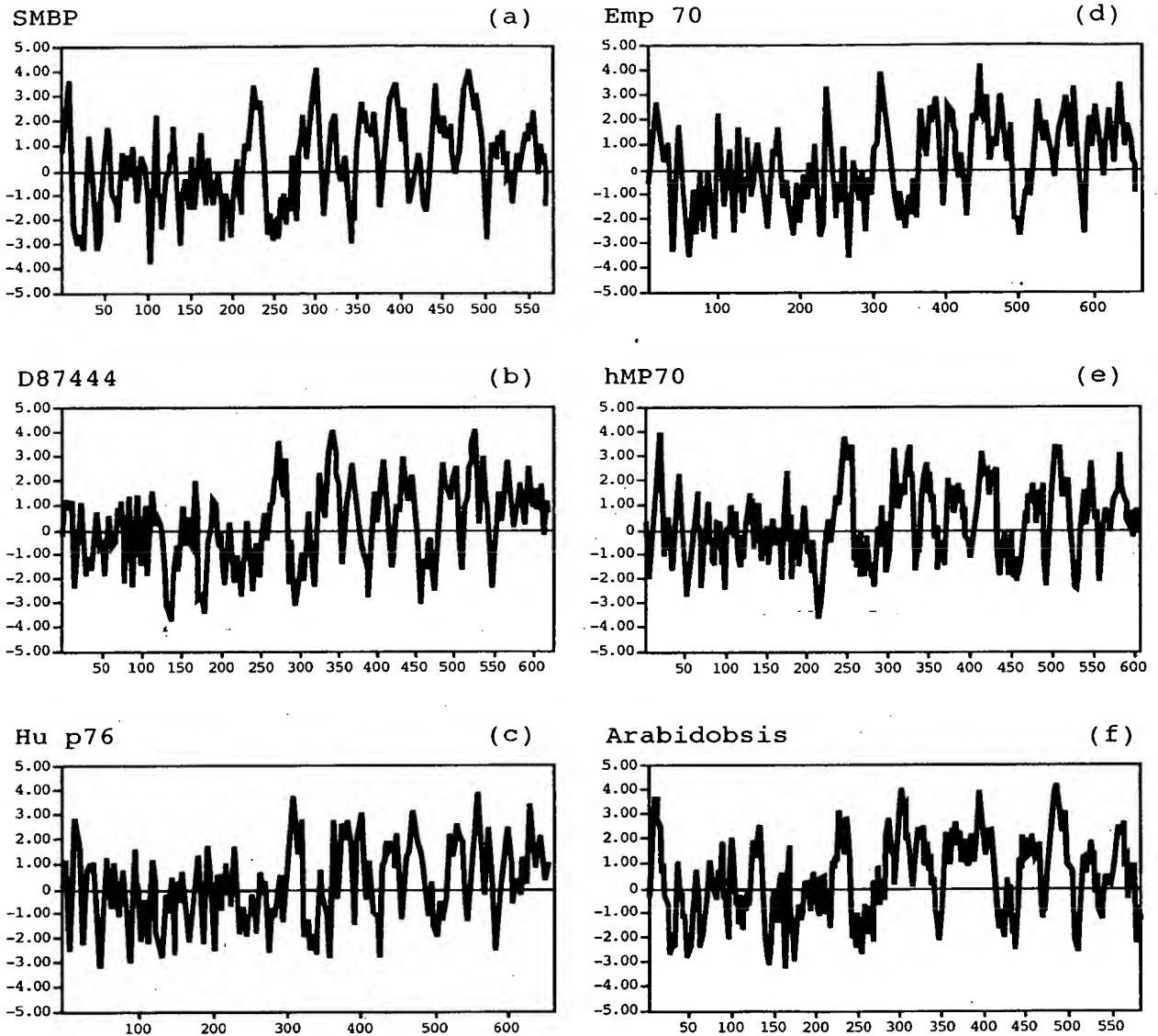


Fig. 23 B

Hydropathy index (Kyte-Doolittle, 1982)

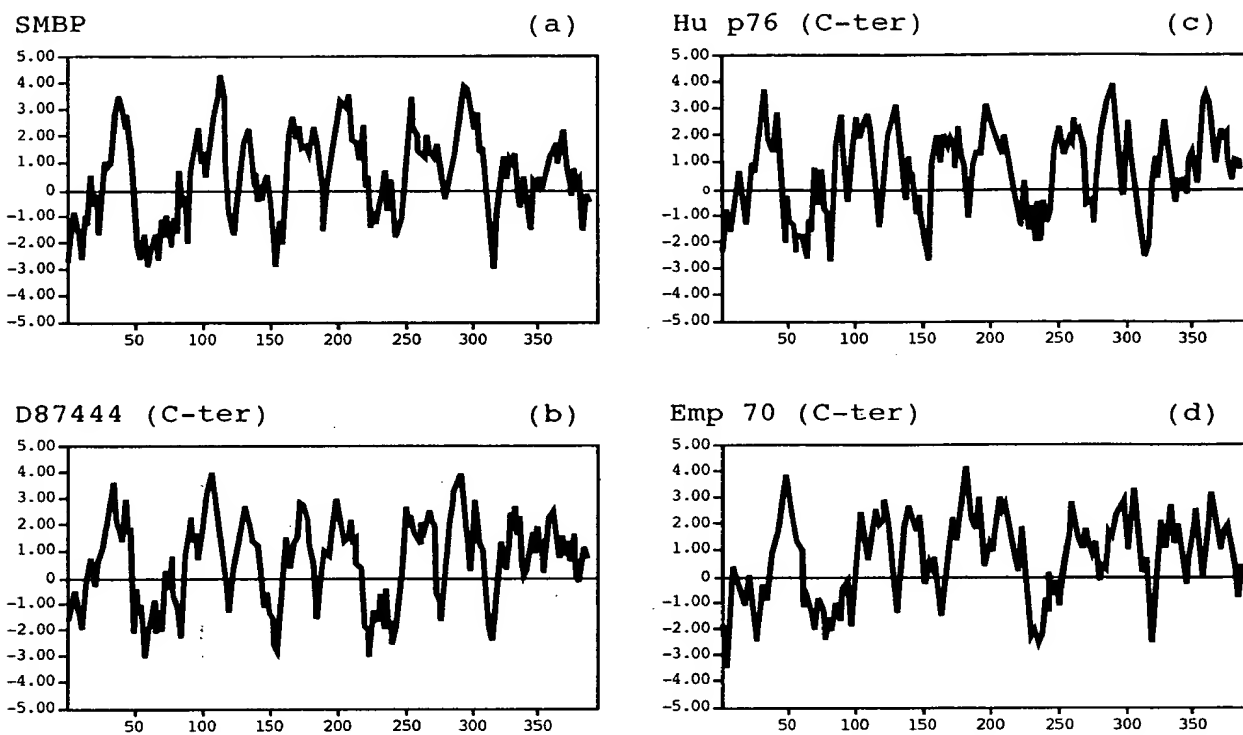


Fig. 24 A

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1      CC GCC GCG CTG TGG CTG CTG CTG CTG CTG CCC CGG ACC CGG GCG GAC GAG CAC GAA CAC ACG TAT CAA GAT 74
1      A  A  L  W  L  L  L  L  L  L  L  P  R  T  R  A  D  E  H  E  H  T  Y  Q  D  24

75    AAA GAG GAA GTT GTC TTA TGG ATG AAT ACT GTT GGG CCC TAC CAT AAT CGT CAA GAA ACA TAT CCG TAC TTT TCA CTT CCA TTC TGT GTG 164
25    K  E  E  V  V  L  W  M  N  T  V  G  P  Y  H  N  R  Q  E  T  Y  K  Y  F  S  L  P  F  C  V  54

165   GGG TCA AAA AAA AGT ATC AGT CAT TAC CAT GAA ACT CTG GGA GAA GCA CTT CAA GGG GTT GAA TTG GAA TTT AGT GGT CTG GAT ATT AAA 254
55    G  S  K  K  S  I  S  H  Y  H  E  T  L  G  E  A  L  Q  G  V  E  L  E  F  S  G  L  D  I  K  84

255   TTT AAA GAT GAT GTG ATG CCA GCC ACT TAC TGT GAA ATT GAT TTA GAT AAA GAA AAG AGA GAT GCA TTT GTA TAT CCC ATA AAA AAT CAT 344
85    F  K  D  D  V  M  P  A  T  Y  C  E  I  D  L  D  K  E  K  R  D  A  F  V  Y  A  I  K  N  H  114

345   TAC TGG TAC CAG ATG TAC ATA GAT GAT TTA CCA ATA TGG GGT ATT GTT GGT GAG GCT GAT GAA AAT GGA GAA GAT TAC TAT CTT TGG ACC 434
115   Y  W  Y  Q  M  Y  I  D  D  L  P  I  W  G  I  V  G  E  A  D  E  N  G  E  D  Y  Y  L  W  T  144

435   TAT AAA AAA CTT GAA ATA GGT TTT AAT GGA AAT CGA ATT GTT GAT GTT AAT CTA ACT AGT GAA GGA AAG GTG AAA CTG CTT CCA AAT ACT 524
145   Y  K  K  L  E  I  G  F  N  G  N  R  I  V  D  V  N  L  T  S  E  G  K  V  K  L  V  P  N  T  174

525   AAA ATC CAG ATG TCA TAT TCA GTA AAA TGG AAA AAC TCA GAT GTG AAA TTT GAA GAT CGA TTT GAC AAA TAT CTT GAT CCG TCC TTT TTT 614
175   K  I  Q  M  S  Y  S  V  K  W  K  K  S  D  V  K  F  E  D  R  F  D  K  Y  L  D  P  S  F  F  204

615   CAA CAT CGG ATT CAT TGG TTT TCA ATT TTC AAC TCC TTC ATG ATG GTG ATC TTC TTG GTG GGC TTA GTT TCA ATG ATT TTA ATG AGA ACA 704
205   Q  E  R  I  H  W  F  S  I  F  N  S  F  M  M  V  I  F  L  V  G  L  V  S  M  I  L  M  R  T  234

705   TTA AGA AAA GAT TAT GCT CGG TAC AGT AAA GAG GAA GAA ATG GAT GAT ATG GAT AGA GAC CTA GGA GAT GAA TAT GGA TGG AAA CAG GTG 794
235   L  R  K  D  Y  A  R  Y  S  K  E  E  E  M  D  D  M  D  R  D  L  G  D  E  Y  G  W  K  Q  V  264

795   CAT GGA GAT GTA TTT AGA CCA TCA AGT CAC CCA CTG ATA TTT TCC TCT CTG ATT GGT TCT GGA TGT CAG ATA TTT GCT GTG TCT CTC ATC 884
265   H  G  D  V  F  R  P  S  S  H  P  L  I  F  S  S  L  I  G  S  G  C  Q  I  F  A  V  S  L  I  294

885   GTT ATT ATT GTT GCA ATG ATA GAA GAT TTA TAT ACT GAG ACG GGA TCA ATG CTC AGT ACA GCC ATA TTT GTG TAT GCT GCT ACG TCT CCA 974
295   V  I  I  V  A  M  I  E  D  L  Y  T  E  R  G  S  M  L  S  T  A  I  F  V  Y  A  A  T  S  P  324

975   GTG AAT GGT TAT TTT GGA GGA AGT CTG TAT GCT AGA CAA GGA GGA AGG AGA TGG ATA AAG CAG ATG TTT ATT GGG GCA TTC CTT ATC CCA 1064
325   V  N  G  Y  F  G  G  S  L  Y  A  R  Q  G  G  R  R  W  I  K  Q  M  F  I  G  A  F  L  I  P  354

1065  CCT ATG GTG TGT GGC ACT GCC TTC TTC ATC AAT TTC ATA GCC ATT TAT TAC CAT GCT TCA AGA GCC ATT CCT TTT GGA ACA ATG GTG GCC 1154
355   A  M  V  C  G  T  A  F  F  I  N  F  I  A  I  Y  Y  H  A  S  R  A  I  P  F  G  T  M  V  A  384

1155  GTT TGT TGC ATC TGT TTT TTT GTT ATT CTT CCT CTA AAT CTT GTT GGT ACA ATA CTT GGC CGA AAT CTG TCA GGT CAG CCC AAC TTT CCT 1244
385   V  C  C  I  C  F  F  V  I  L  P  L  N  L  V  G  T  I  L  G  R  N  L  S  G  Q  P  N  F  P  414

1245  TGT GGT GTC AAT GCT GTG CCT CGT CCT ATA CCG GAG AAA AAA TGG TTC ATG GAG CCT GCG GTT ATT GTT TGC CTG GGT GGA ATT TTA CCT 1334
415   C  R  V  N  A  V  P  R  P  I  P  E  K  K  W  F  M  E  P  A  V  I  V  C  L  G  G  I  L  P  444

1335  TTT GGT TCA ATC TTT ATT GAA ATG TAT TTC ATC TTC ACG TCT TTC TGG GCA TAT AAG ATC TAT TAT GTC TAT GGC TTC ATG ATG CTG GTG 1424
445   F  G  S  I  F  I  E  M  Y  F  I  F  T  S  F  W  A  Y  K  I  Y  Y  V  Y  G  F  M  M  L  V  474

1425  CTG GTT ATC CTG TGC ATT GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT GCA GAA GAT TAC CGG TGG CAA TGG ACA 1514
475   L  V  I  L  C  I  V  T  V  C  V  T  I  V  C  T  Y  F  L  L  N  A  E  D  Y  R  W  Q  W  T  504

1515  AGT TTT CTC TCT GCT GCA TCA ACT GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA ACA AAG ATG TAT GGC TTA TTT 1604
505   S  F  L  S  A  A  S  T  A  I  Y  V  Y  M  Y  S  F  Y  Y  Y  F  F  K  T  K  M  Y  G  L  F  534

1605  CAA ACA TCA TTT TAC TTT GGA TAT ATG CCG GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT GGT TAC ATG GGA ACA AGT TTT 1694
535   Q  T  S  F  Y  F  G  Y  M  A  V  F  S  T  A  L  G  I  M  C  G  A  I  G  Y  M  G  T  S  A  564

1695  TTT GTC CGA AAA ATC TAT ACT AAT CTG AAA ATT GAC TAG AGACCAAGAAAACCTGGAACCTTGATCAATTCTTTTCATAGGGTGAACCTGCACAGCAAAA 1800
565   F  V  R  K  I  Y  T  N  V  K  I  D  576

```

Fig. 24 B

